

IN THE CLAIMS:

This listing of claims will replace all prior versions, and listings, of claims in the application:

1 - 5. (Canceled)

6. (Currently amended) A method for identifying [[a]] at least one protein that is differentially displayed in [[the]] mass spectra of two complex biologic samples, the method comprising the steps of:

(a) in parallel, adsorbing separately a subset of proteins from each of the two complex biologic samples to an adsorptive surface of [[an]] at least one affinity capture probe;

(b) ~~detecting~~ determining the mass of at least one protein that is differentially displayed in the laser desorption ionization (LDI) mass spectra of the two adsorbed subsets of proteins;

(c) in parallel, cleaving at least a portion of the two adsorbed subsets of proteins ~~adsorbed to said probes into to create~~ protein cleavage products in two cleaved subsets; [[and]]

(d) detecting at least one protein cleavage products
product that ~~[[are]]~~ is differentially displayed in LDI mass
spectra of the two cleaved ~~adsorbed~~ subsets;

(e) characterizing at least one of the differentially
displayed protein cleavage products detected in step (d) by
tandem mass spectrometry;

~~(d)~~ (f) for each differentially displayed protein
cleavage product characterized in step (e), determining
identifying at least one identity candidate protein that
includes the characteristics of that protein cleavage product
as determined in step (e), and determining the predicted mass
of the at least one candidate protein ~~for at least one~~
~~differentially displayed protein cleavage product with a tandem~~
~~mass spectrometer; and~~

~~(e)~~ (g) correlating the predicted mass of at least
one of the identity candidate proteins identified in step (f)
~~for the at least one differentially displayed protein cleavage~~
~~product of step (d) with~~ the mass of at least one of the ~~[[a]]~~
differentially displayed proteins determined in ~~[[of]]~~ step
(b) ,

whereby ~~the correlation~~ a correspondence between the
predicted mass of one of the candidate proteins identified in
step (f) and the mass of one of the differentially displayed
proteins determined in step (b) identifies ~~[[a]]~~ the
differentially displayed protein as the candidate protein as
~~had been differentially present in the two complex biologic~~
~~samples.~~

7-8. (Canceled)

9. (Currently amended) The method of claim 6 [[or 7]] wherein at least one of the differentially displayed proteins of step (b) is detectable uniquely in one of said two complex biologic samples.

10. (Currently amended) The method of claim 6 [[or 7]] wherein [[(c)]] the cleaving of step (c) comprises enzymatic fragmentation.

11. (Currently amended) The method of claim 10 wherein the enzymatic fragmentation comprises ~~comprising~~ limited enzymatic digestion.

12. (Currently amended) The method of claim 6 [[or 7]] wherein [[(c)]] the cleaving of step (c) comprises chemical cleavage.

13. (Currently amended) The method of claim 12 wherein the chemical cleavage comprises acid hydrolysis.

14. (Currently amended) The method of claim 6 [[or 7]] wherein the two complex biologic samples are selected from the group consisting of: (1) a sample from a healthy source and a sample from a diseased source, (2) a sample from a test model exposed to a toxic compound and a sample from a test model not exposed to the toxic compound [[or]] , and (3) a sample from a subject that responds to a drug and a sample from a subject that does not respond to the drug.

15 - 26. (Canceled)

27. (New) The method of claim 6, wherein:

characterizing step (e) comprises the step of determining by tandem mass spectrometry at least a portion of the amino acid sequence for at least one of the differentially displayed protein cleavage products detected in step (d); and

identifying step (f) comprises the step of identifying at least one candidate protein that includes the amino acid sequence determined in step (e) and determining the predicted mass of the at least one candidate protein.

28. (New) The method of claim 6, wherein:

characterizing step (e) comprises the step of determining by tandem mass spectrometry at least one tandem

mass spectra for at least one of the differentially displayed protein cleavage products detected in step (d); and

identifying step (f) comprises the step of identifying at least one candidate protein whose predicted tandem mass spectrum corresponds to at least one of the tandem mass spectra determined in step (e) and determining the predicted mass of the at least one candidate protein.